

#4

RAW SEQUENCE LISTING DATE: 12/19/2000
 PATENT APPLICATION: US/09/724,583 TIME: 16:58:07

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3 <110> APPLICANT: Saris, Christiaan M.
4     Giles, Jennifer
5     Mu, Sharon X.
6     Xia, Min
7     Bass, Michael B.
8     Craveiro, Roger
10 <120> TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
11     Uses Thereof
13 <130> FILE REFERENCE: 00-1213
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/724,583
C--> 16 <141> CURRENT FILING DATE: 2000-11-28
18 <150> PRIOR APPLICATION NUMBER: 60/170,191
19 <151> PRIOR FILING DATE: 1999-12-10
21 <150> PRIOR APPLICATION NUMBER: 60/188,053
22 <151> PRIOR FILING DATE: 2000-03-09
24 <150> PRIOR APPLICATION NUMBER: 60/194,521
25 <151> PRIOR FILING DATE: 2000-04-04
27 <150> PRIOR APPLICATION NUMBER: 60/195,910
28 <151> PRIOR FILING DATE: 2000-04-10
30 <160> NUMBER OF SEQ ID NOS: 37
32 <170> SOFTWARE: PatentIn Ver. 2.0
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 1020
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
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40 <221> NAME/KEY: CDS
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46 gga atg tgt tcc ctc ccc atg gca aga tac tac ata att aaa tat gca 108
47 Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala
48 1 5 10 15
50 gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gal 156
51 Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp
52 20 25 30
54 cct gtt gca gac aac tgc tgt gca gag aag atc tgc aca ctt cct aac 204
55 Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn
56 35 40 45
58 aga ggc ttg gac cgc acc aag gtc ccc att ttc ctg ggg atc cag gga 252
59 Arg Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly
60 50 55 60
62 ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc cta 300
63 Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Gln Gly Pro Ser Leu
64 65 70 75
66 cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag 348
67 Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu

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70 gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc agg 396
71 Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg
72          100          105          110
74 ctt gag get get gcc tgg cct ggc tgg ttc ctg tgt ggc ccg gca gag 444
75 Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
76          115          120          125
78 ccc cag cag cca gta cag ctc acc aaq gag agt gag ecc tca gcc cgt 492
79 Pro Gln Gln Pro Val Gln Leu Thr Lys Gln Ser Glu Pro Ser Ala Arg
80          130          135          140
82 acc aaq ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttL 542
83 Thr Lys Phe Tyr Phe Glu Gln Ser Trp
84          145          150
86 tagccttgtg cccccaacc aagctcctcc tctcagggt ctatggtagg cagaataatg 602
88 tccccgaaa tatgtccaca tctaatccc aagatctgtg catatgttac catacatgtc 662
90 caaaagqgtt ttgcaaatgt gattatgtta aqgatcttga aatgaggaga caatectggg 722
92 ttatccttgt gggctcagtt taatcacaaq aaggaggcag gaaggagagag tcagagagag 782
94 aatggaagat accatgcttc taattttgaa gatggagtga ggggccttga gccacaaaat 842
96 gcaggtgttt ttagaaggtg gaaaagccaa yggaaaggat tctcctctag agtctccgga 902
98 aqgaacacag ctcttgacac atggaattca gctcagtgac acccatttca gacttctgac 962
100 ctccacaact ataaaaaat aaacttgtgt tattgtaaac ctctaaaaaa aaaaaaaa 1020
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105 <212> TYPE: PRT
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112 Glu Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp Pro
113 20 25 30
115 Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn Arg
116 35 40 45
118 Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly
119 50 55 60
121 Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Gln Gly Pro Ser Leu Gln
122 65 70 75 80
124 Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu Ala
125 85 90 95
127 Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg Leu
128 100 105 110
130 Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro
131 115 120 125
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136 Lys Phe Tyr Phe Glu Gln Ser Trp
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140 <210> SEQ ID NO: 3
141 <211> LENGTH: 1020
142 <212> TYPE: DNA

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143 <213> ORGANISM: Homo sapiens
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147 <222> LOCATION: (64)..(522)
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152 gga atg tgt tcc ctc ccc atg qca aqa tac tac ata att aaa tat gca 108
153 Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala
154 1 5 10 15
156 gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gat 156
157 Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp
158 20 25 30
160 cct gtt qca gac aac tgc tgt qca gag aag atc tgc ata ctt cct aac 204
161 Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu Pro Asn
162 35 40 45
164 aga ggc ttg gcc cgc acc aag qtc ccc att ttc ctg ggg atc cag qga 252
165 Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly
166 50 55 60
168 ggg agc cgc tgc ctg qca tgt gtg gag aca gaa gag ggg cct tcc cta 300
169 Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu
170 65 70 75
172 cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag 348
173 Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu
174 80 85 90 95
176 gcc aca cgc ttc acc ttc cag agc agc tca ggc tcc gcc ttc aag 396
177 Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg
178 100 105 110
180 ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc cag qca gag 444
181 Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
182 115 120 125
184 ccc cag cag cca gta caa ctc acc aag gag agt qag ccc tca gcc cgt 492
185 Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg
186 130 135 140
188 acc aag ttt tac ttt gaa cag agc tgg taq ggagacagga aactgcgttt 542
189 Thr Lys Phe Tyr Phe Glu Gln Ser Trp
190 145 150
192 tagcctttgtg ccccccaccc aaqctcctcc tgcctcagggt ctatggtagg cagaataatg 602
194 tcccccgaaa tatgtccaca tccctaatccc aagatctgtg catatgttcc catacatgtc 662
196 caaagagggtt ttgcaaatgt gatttatgtta aggatcttga aatgaggaga caatcctggg 722
198 ttatccttgt ggqctcagtt taatcacaag aaggaggcag gaaggagagag tcagagagag 782
200 aatggaagat accatgcttc taattttgaa gatggagtga ggggccttga gccacacaaat 842
202 gcagggtgtt ttagaagggt gaaaagccaa ggaacggat tctcctctag agtctccgga 902
204 aggaacacag ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac 962
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212 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 4

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215 Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala Asp
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218 Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp Pro
219      20              25              30
221 Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu Pro Asn Arg
222      35              40              45
224 Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly
225      50              55              60
227 Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu Gln
228      65              70              75              80
230 Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu Ala
231      85              90              95
233 Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg Leu
234      100             105             110
236 Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro
237      115             120             125
239 Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg Thr
240      130             135             140
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259 Met Val Leu Ser Gly Ala Leu Cys Phe Arg Glu Asp Glu Thr Pro Leu
260      1              5              10              15
262 att gca gga atg tgt tcc ctc ccc atg gca aca tac tac ata att aaa 153
263 Ile Ala Gly Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys
264      20              25              30
266 tat gca gac cag aag gct cta tac aca aca gat ggc cag ctg ctg ctg 201
267 Tyr Ala Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val
268      35              40              45
270 gga gat cct gtt gca gac aac tgc tgt gca gag aag atc tgc ata ctt 249
271 Gly Asp Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu
272      50              55              60
274 cct aac aga ggc ttg gcc cgc acc aag gtc ccc att ttc ctg ggg atc 297
275 Pro Asn Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile
276      65              70              75              80
278 cag gga ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct 345
279 Gln Gly Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro
280      85              90              95
282 tcc cta cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt 393
283 Ser Leu Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly

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286 gaa gag gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc 441
287 Glu Glu Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala
288          115          120          125
290 ttc agg ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg 489
291 Phe Arg Leu Glu Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro
292          130          135          140
294 qca gag ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca 537
295 Ala Glu Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser
296 145          150          155          160
298 gcc cgt acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga 583
299 Ala Arg Thr Lys Phe Tyr Phe Glu Gln Ser Trp
300          165          170
302 aactgcggttt taqcttctgtg cccccaacc aagctcatcc tgctcagggt ctatggtatgg 643
304 cagaataatg tcccccaaa tatgtccaca tccataatccc aagatctgtg catalgttac 703
306 catacatgtc caaagaggtt ttqcaaatgt gattatgtta a 744
309 <210> SEQ ID NO: 6
310 <211> LENGTH: 171
311 <212> TYPE: PRT
312 <213> ORGANISM: Homo sapiens
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318 Ile Ala Gly Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys
319 20 25 30
321 Tyr Ala Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val
322 35 40 45
324 Gly Asp Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu
325 50 55 60
327 Pro Asn Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile
328 65 70 75 80
330 Gln Gly Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro
331 85 90 95
333 Ser Leu Gln Leu Glu Asp Val Asn Ile Glu Gln Leu Tyr Lys Gly Gly
334 100 105 110
336 Glu Glu Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala
337 115 120 125
339 Phe Arg Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro
340 130 135 140
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351 <212> TYPE: PRT
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VERIFICATION SUMMARY DATE: 12/19/2000
PATENT APPLICATION: US/09/724,583 TIME: 16:58:08

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date